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Scientific and Technical Information Center

SEARCH REQUEST FORM

Requester's Full Name: JANE ZARA Examiner #: 77572 Date: 11-30-07

Art Unit: 1635 Phone Number: 2-0765 Serial Number: 10/626,879

Location (Bldg/Room#): 2A59 (Mailbox #): 2C18 Results Format Preferred (circle): PAPER DISK

****

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: Mol'l Small Stage RNA...

Inventors (please provide full names): J. Han et al

Earliest Priority Date: 7/25/03

Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

For Sequence Searches Only ***Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.***

Please Search Seq ID Nos 1 & 2.
Size limit to 100 NTS.

Please Search Seq ID Nos 1 & 2.
Size limit to 40 NTS.

Please Include Interference Search.
Thanks

****

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Searcher: _____

Searcher Phone #: _____

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Date Searcher Picked Up: _____

Date Completed: _____

Searcher Prep & Review Time: _____

Online Time: _____

Type of Search

_____ NA Sequence (#)

_____ AA Sequence (#)

_____ Structure (#)

_____ Bibliographic

_____ Litigation

_____ Fulltext

_____ Other

Vendors and cost where applicable

_____ STN _____ Dialog

_____ Questel/Orbit _____ Lexis/Nexis

_____ Westlaw _____ WWW/Internet

____In-house sequence systems

___Commercial ____Oligomer _____Score/Length

___ Interference ____ SPDI _____ Encode/Transl

_____ Other (specify)

ACCESS DB # _____

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Scientific and Technical Information Center

SEARCH REQUEST FORM

Requester's Full Name: JANE ZARA Examiner #: 77512 Date: 9/18/07
Art Unit: 1635 Phone Number: 2-0764 Serial Number: 10/626,879
Location (Bldg/Room#): 2A59 (Mailbox #): 2C18 Results Format Preferred (circle): ~~PAPER~~ DISK
****

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: Mod'l Small interfering RNAi

Inventors (please provide full names): G. HAN et al.

Earliest Priority Date: 7/25/03

Search Topic:
Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

For Sequence Searches Only ***Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.***

Please Search Seq ID No: 9

Size limit to 50 NTS.

****

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Searcher: _____
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Searcher Prep & Review Time: _____
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Type of Search

_____ NA Sequence (#)
_____ AA Sequence (#)
_____ Structure (#)
_____ Bibliographic
_____ Litigation
_____ Fulltext
_____ Other

Vendors and cost where applicable

_____ STN _____ Dialog
_____ Questel/Orbit _____ Lexis/Nexis
_____ Westlaw _____ WWW/Internet
_____ In-house sequence systems
___ Commercial ___ Oligomer ___ Score/Length
___ Interference ___ SPDI ___ Encode/Transl
_____ Other (specify)

GenCore version 6.2.1

OM nucleic - nucleic search, using sw model

Run on: September 21, 2007, 14:21:44 ; Search time 441 Seconds
(without alignments)
6435.935 Million cell updates/sec

Title: US-10-626-879-9
Perfect score: 383
Sequence: 1 gccagcccccgauuggggggc.....aaagaaaaaccaaacguaac 383

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 5640290

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_200701:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*

4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*
16: geneseqn2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	48.4	12.6	50	4	AAC92382	Aac92382 Oligonucl
	2	48	12.5	48	2	AAZ23541	Aaz23541 HCV DNA f
	3	47	12.3	47	8	ABZ81791	Abz81791 HCV 5' UT
	4	46.8	12.2	50	13	ADS34712	Ads34712 siRNA-9 P
c	5	45	11.7	45	13	ADR47301	Adr47301 Caenorhab
	6	44.8	11.7	48	2	AAZ23542	Aaz23542 Human DNA
	7	44.4	11.6	46	2	AAV54438	Aav54438 Nucleotid
	8	44	11.5	44	3	AAA50912	Aaa50912 Nucleic a
	9	43	11.2	47	12	ADP87770	Adp87770 Extended
	10	42	11.0	42	2	AAV15321	Aav15321 Hepatitis
	11	42	11.0	42	2	AAX60959	Aax60959 Hepatitis

	11	42	11.0	42	2	AAX60959	Aax60959 Hepatitis
	12	42	11.0	42	15	AEF39282	Aef39282 HCV 224 t
	13	42	11.0	49	14	ADW28911	Adw28911 Wild type
c	14	41.4	10.8	45	2	AAT09177	Aat09177 Hepatitis
c	15	41.4	10.8	45	2	AAV20718	Aav20718 Hepatitis
c	16	41.4	10.8	45	2	AAV22770	Aav22770 Capture/A
c	17	41.4	10.8	45	6	ABK86839	Abk86839 Human imm
c	18	41.4	10.8	45	8	AAD56316	Aad56316 Hepatitis
c	19	41.4	10.8	45	12	ADQ74916	Adq74916 HCV Captu
c	20	41.4	10.8	45	14	AEB17468	Aeb17468 HCV 5'UTR
c	21	41.4	10.8	45	14	AEB54512	Aeb54512 HCV detec
	22	41	10.7	41	2	AAX37635	Aax37635 HCV detec
	23	41	10.7	41	6	ABK52637	Abk52637 Minority
	24	41	10.7	41	6	ABK52638	Abk52638 Minority
c	25	41	10.7	41	6	AAL40116	Aal40116 Pathogeni
	26	40.4	10.5	49	14	ADW28990	Adw28990 Hepatitis
	27	40.4	10.5	49	14	ADW28992	Adw28992 Hepatitis
	28	40.4	10.5	49	14	ADW28994	Adw28994 Hepatitis
	29	40.4	10.5	49	14	ADW28988	Adw28988 Hepatitis
c	30	40.2	10.5	45	2	AAQ32626	Aaq32626 HCV antig
	31	40	10.4	40	2	AAQ32627	Aaq32627 HCV antig
	32	40	10.4	40	2	AAV54434	Aav54434 Nucleotid
c	33	40	10.4	40	2	AAV54436	Aav54436 Nucleotid
	34	40	10.4	40	3	AAA86970	Aaa86970 Probe for
	35	40	10.4	40	3	AAA93199	Aaa93199 Hepatitis
	36	40	10.4	40	10	ADC46967	Adc46967 Synthesis
	37	40	10.4	40	12	ADP87774	Adp87774 TEX contr
	38	40	10.4	40	12	ADP87786	Adp87786 TEX synth
	39	39.4	10.3	41	11	ADM68241	Adm68241 Directed
	40	39.4	10.3	41	12	ADP87819	Adp87819 HCV fragm
c	41	39	10.2	39	2	AAX37633	Aax37633 HCV detec
c	42	39	10.2	39	13	ADR82689	Adr82689 Peptide n
c	43	39	10.2	39	13	ADR82699	Adr82699 Peptide n
c	44	39	10.2	39	13	ADR82698	Adr82698 Peptide n

c	44	39	10.2	39	13	ADR82698	Adr82698	Peptide n
	45	38.8	10.1	49	14	ADW28909	Adw28909	Wild type

ALIGNMENTS

RESULT 1
AAC92382/c
ID AAC92382 standard; DNA; 50 BP.
XX
AC AAC92382;
XX
DT 26-MAR-2001 (first entry)
XX
DE Oligonucleotide sequence SEQ ID NO:10.
XX
KW Amplification; analysis; RNA transcription; RNA polymerase; detection;
KW bacterium; virus; foodstuff; soil; environmental water; seawater;
KW house dust; ss.
XX
OS Synthetic.
XX
PN WO200075371-A1.
XX
PD 14-DEC-2000.
XX
PF 05-JUN-2000; 2000WO-JP003647.
XX
PR 04-JUN-1999; 99JP-00157653.
XX
PA (TOYJ) TOSOH CORP.
XX
PI Ishiguka T, Ishigure T, Saitoh J, Sakai T;

PI Ishizuka T, Ishiguro T, Saitoh J, Sakai T;
XX
DR WPI; 2001-061738/07.
XX
PT Potentiated method for amplification of nucleic acids for detection in
PT biological samples.
XX
PS Example 4; Page 40; 42pp; Japanese.
XX
CC The present invention describes a method for amplifying a specific RNA
CC from a sample. The method comprises generating from the template RNA in
CC the sample a two-stranded DNA, which contains sequences complementary to
CC and homologous with the RNA sequence, and a transcription promoter. RNA
CC is transcribed from the two-stranded DNA using an RNA polymerase, in as
CC reaction mixture comprising inosine triphosphate (ITP), Adenosine
CC triphosphate (ATP), uridine triphosphate (UTP), cytidine triphosphate
CC (CTP) and guanosine triphosphate (GTP), and the reaction cycle is
CC repeated as necessary. The method can be used for the detection and assay
CC of specific RNA sequences, such as those occurring in bacteria and
CC viruses, in samples such as foodstuffs, soil, environmental waters,
CC seawater and house dust. The addition of ITP increases the efficiency of
CC the amplification reaction. The present sequence represents an
CC oligonucleotide used in an example from the present invention, for the
CC exemplification of the method of the invention
XX
SQ Sequence 50 BP; 11 A; 14 C; 18 G; 7 T; 0 U; 0 Other;

Query Match 12.6%; Score 48.4; DB 4; Length 50;
Best Local Similarity 78.0%; Pred. No. 0.00018;
Matches 39; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 83 CCAUGGCGUUAGUAUGAGUGUCGUGCAGCCUCCAGGACCCCCCCUCCCGG 132
       |||:||||::||:|:|||:|: |:||||||:||||||||||||||:|||||
Db 50 CCATCCCCTTACTATCACTCTTCTCCACCCTCCACCACCCCCCTCCCCC 1

```
Db         50 CCATGGCGTTAGTATGAGTGTTGTGCAGCCTCCAGGACCCCCCCTCCCGG 1


RESULT 2
AAZ23541
ID   AAZ23541 standard; DNA; 48 BP.
XX
AC   AAZ23541;
XX
DT   21-DEC-1999  (first entry)
XX
DE   HCV DNA fragment 1.
XX
KW   Assay; amplification; hybridisation; probe; detection; viral; bacterial;
KW   cellular; yeast; fungal; primer; ss.
XX
OS   Hepatitis C virus.
XX
PN   DE19814828-A1.
XX
PD   07-OCT-1999.
XX
PF   02-APR-1998;   98DE-01014828.
XX
PR   02-APR-1998;   98DE-01014828.
XX
PA   (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX
PI   Kessler C,  Haberhausen G,  Batz H,  Oerum H;
XX
DR   WPI; 1999-552286/47.
XX
PT   Nucleic acid amplification assay for detecting viral, bacterial,
PT   cellular, yeast or fungal nucleic acids
```

PT cellular, yeast or fungal nucleic acids.
XX
PS Disclosure; Fig 4; 28pp; German.
XX
CC This invention describes a novel assay for a nucleic acid comprises: (a)
CC generating amplification products from a fragment of the nucleic acid,
CC (b) contacting the amplification products with a probe; and (c) detecting
CC hybridization between the amplification product and the probe. The assay
CC is useful for detection of viral, bacterial, cellular, yeast or fungal
CC nucleic acids in human, animal, bacterial, plant, yeast or fungal
CC samples, e.g. feces, smears, cell suspensions, cultures or tissue, cell
CC or liquid biopsy samples. This sequence represents a fragment of the HCV
CC genome used in the method of the invention
XX
SQ Sequence 48 BP; 9 A; 18 C; 14 G; 7 T; 0 U; 0 Other;

Query Match 12.5%; Score 48; DB 2; Length 48;
Best Local Similarity 85.4%; Pred. No. 0.00024;
Matches 41; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

```
Qy          93 AGUAUGAGUGUCGUGCAGCCUCCAGGACCCCCCCUCCCGGGAGAGCCA 140
               ||:|:|||:|:||:||||||:|||||||||||||:||||||||||||
Db           1 AGTATGAGTGTCGTGCAGCCTCCAGGACCCCCCCTCCCGGGAGAGCCA 48
```

RESULT 3
ABZ81791
ID ABZ81791 standard; RNA; 47 BP.
XX
AC ABZ81791;
XX
DT 11-JUN-2003 (first entry)
XX
DE HCV 5' UTR molecular interaction site 7 polynucleotide 2

```
DE   HCV 5' UTR molecular interaction site 7 polynucleotide 2.
XX
KW   HCV; 5' untranslated region; 5' UTR; molecular interaction;
KW   secondary structure; combinatorial library; screening; virucide; ss.
XX
OS   Hepatitis c virus.
XX
FH   Key             Location/Qualifiers
FT   misc_binding    1. .4
FT                   /*tag=  a
FT                   /bound_moiety= "Polynucleotide 1"
FT                   /note= "forms double-stranded region with bases 14-17 of
FT                   sequence in ABZ81790"
FT   misc_structure  5
FT                   /*tag=  b
FT                   /note= "forms internal loop with base 13 of sequence in
FT                   ABZ81790"
FT   misc_binding    6. .7
FT                   /*tag=  c
FT                   /bound_moiety= "Polynucleotide 1"
FT                   /note= "forms double-stranded region with bases 11-12 of
FT                   sequence in ABZ81790"
FT   stem_loop       8. .19
FT                   /*tag=  d
FT   misc_binding    20. .21
FT                   /*tag=  e
FT                   /bound_moiety= "Bases 30-31"
FT                   /note= "forms double-stranded stem region with bases 30-
FT                   31"
FT   misc_structure  22. .29
FT                   /*tag=  f
FT                   /note= "internal loop"
FT   misc_binding    23. .28
FT                   /*tag=  g
```

```
FT                   /*tag=  g
FT                   /bound_moiety= "Bases 42-47"
FT                   /note= "forms double-stranded dangling structure"
FT   misc_binding    30. .31
FT                   /*tag=  h
FT                   /bound_moiety= "Bases 20-21"
FT                   /note= "forms double-stranded stem region with bases 20-
FT                   21"
FT   misc_binding    32. .40
FT                   /*tag=  i
FT                   /bound_moiety= "Polynucleotide 1"
FT                   /note= "forms double-stranded region with bases 2-10 of
FT                   sequence in ABZ81790"
FT   misc_binding    42. .47
FT                   /*tag=  g
FT                   /bound_moiety= "Bases 23-28"
FT                   /note= "forms double-stranded dangling structure"
XX
PN   WO2003018747-A2.
XX
PD   06-MAR-2003.
XX
PF   19-AUG-2002; 2002WO-US026219.
XX
PR   22-AUG-2001; 2001US-0314236P.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Ecker DJ;
XX
DR   WPI; 2003-300721/29.
XX
PT   Polynucleotides useful for screening combinatorial libraries of compounds
PT   that inhibit or stimulate viral replication, comprise molecular
```

PT that inhibit or stimulate viral replication, comprise molecular
PT interaction sites of hepatitis C virus RNA having a defined secondary
PT structure.
XX
PS Claim 26; Page 38; 63pp; English.
XX
CC The present sequence is that of the second polynucleotide of a molecular
CC interaction site (number 7) that has been identified in the 5'
CC untranslated region (5' UTR) of hepatitis C virus (HCV) RNA (see
CC ABZ81793). The first polynucleotide forming site 7 is given in ABZ81790.
CC The 2 polynucleotides together form a double-stranded RNA including
CC internal and terminal loops and 2 dangling structures. The 8 molecular
CC interaction sites identified in the HCV 5' UTR each have a secondary
CC structure capable of interacting with cellular components, such as
CC factors and proteins required for translation and other cellular
CC processes. Nucleic acid molecules, polynucleotides or oligonucleotides
CC comprising the molecular interaction sites can be used to screen,
CC virtually or actually, combinatorial libraries of compounds that bind to
CC them. Such compounds can be used to modulate the activity of HCV RNA and
CC hence to modulate (inhibit or stimulate) viral replication. Thus, novel
CC drugs, and agricultural and industrial chemicals, that operate through
CC the modulation of HCV RNA can be identified
XX
SQ Sequence 47 BP; 6 A; 11 C; 18 G; 0 T; 12 U; 0 Other;

Query Match 12.3%; Score 47; DB 8; Length 47;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 284 UGGUACUGCCUGAUAGGGUGCUUGCGAGUGCCCCGGGAGGUCUCGUA 330
||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 UGGUACUGCCUGAUAGGGUGCUUGCGAGUGCCCCGGGAGGUCUCGUA 47

RESULT 4
ADS34712
ID   ADS34712 standard; DNA; 50 BP.
XX
AC   ADS34712;
XX
DT   02-DEC-2004 (first entry)
XX
DE   siRNA-9 PCR product, seq id 55.
XX
KW   Virucide; antiinflammatory; hepatotropic; hepatitis C virus; HCV;
KW   proliferation; siRNA; short interfering RNA; RNA interference;
KW   gene silencing; ds.
XX
OS   Unidentified.
XX
PN   WO2004078974-A1.
XX
PD   16-SEP-2004.
XX
PF   23-JAN-2004; 2004WO-JP000605.
XX
PR   24-JAN-2003; 2003JP-00016750.
XX
PA   (TOKM-) TOKYO METROPOLITAN ORG MEDICAL RES.
PA   (CHUS) CHUGAI SEIYAKU KK.
XX
PI   Kohara M, Watanabe T, Taira K, Miyagishi M, Sudo M;
XX
DR   WPI; 2004-662428/64.
XX
PT   New oligo ribonucleotide or peptide nucleic acid capable of sequence-
PT   specifically binding with RNA of hepatitis C virus, useful for inhibiting

PT specifically binding with RNA of hepatitis C virus, useful for inhibiting
PT proliferation of hepatitis C virus and useful as hepatitis C virus
PT therapeutic agent.
XX
PS Example 6; SEQ ID NO 55; 80pp; Japanese.
XX
CC The invention relates to an oligo ribonucleotide or peptide nucleic acid
CC (I) capable of sequence-specifically binding with RNA of hepatitis C
CC virus (HCV), and comprising a sequence hybridising under stringent
CC conditions with RNA of HCV. The method of the invention relates to the
CC inhibition of the proliferation of HCV. The oligo ribonucleotide or
CC peptide nucleic acid of the invention is useful for inhibiting the
CC proliferation of HCV which involves contacting (I) with RNA of HCV. (I)
CC is useful as a therapeutic agent of hepatitis C. The current sequence
CC represents a PCR product from an example of the invention.
XX
SQ Sequence 50 BP; 13 A; 14 C; 14 G; 9 T; 0 U; 0 Other;

Query Match 12.2%; Score 46.8; DB 13; Length 50;
Best Local Similarity 80.0%; Pred. No. 0.00055;
Matches 40; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

Qy 309 GAGUGCCCCGGGAGGUCUCGUAGACCGUGCACCAUGAGCACGAAUCCUAA 358
||||:|||||||||||:|:||:|||||||:||| ||:|||||| ||:||:||
Db 1 GAGTGCCCCGGGAGGTCTCGTAGACCGTGCATCATGAGCACAAATCCTAA 50

RESULT 5
ADR47301/c
ID ADR47301 standard; RNA; 45 BP.
XX
AC ADR47301;
XX
DT 18-NOV-2004 (first entry)

DT 18-NOV-2004 (first entry)
XX
DE Caenorhabditis elegans holocentric protein (HCP) oligo, RNA-HCP (X-Y-Z).
XX
KW self assembling oligonucleotide; binding target RNA; gene detection; ss.
XX
OS Caenorhabditis elegans.
OS Synthetic.
XX
PN JP2004242585-A.
XX
PD 02-SEP-2004.
XX
PF 14-FEB-2003; 2003JP-00036013.
XX
PR 14-FEB-2003; 2003JP-00036013.
XX
PA (SANK-) SANKO JUNYAKU CO LTD.
XX
DR WPI; 2004-629600/61.
XX
PT Self assembling oligonucleotides, by using splicing probe having region
PT for binding target RNA, splicing target RNA using ribonuclease,
PT synthesizing RNA fragment with required region of target RNA for self-
PT assembling oligonucleotides.
XX
PS Example; SEQ ID NO 5; 27pp; Japanese.
XX
CC The invention relates to a novel method for self assembling
CC oligonucleotides. The method comprises: using a splicing probe, which
CC comprises a region for binding target RNA; splicing the target RNA bound
CC to the probe using a ribonuclease; synthesising an RNA fragment
CC containing a required region of the target RNA, and self-assembling the
CC oligonucleotides using the above obtained RNA fragment. The invention

CC oligonucleotides using the above obtained RNA fragment. The invention
CC further comprises self-assembled oligonucleotides, obtained by the above
CC method. The method is useful for self-assembling oligonucleotides. The
CC method is useful for detecting a gene, which involves carrying out the
CC method, and detecting the target DNA by detecting the self-assembled
CC oligonucleotides. The method is efficient and requires no special machine
CC and special reagents. The method also provides a low-cost and convenient
CC gene detection method, without using a machine and is uncomplicated. This
CC polynucleotide sequence represents an oligoused in the exemplification of
CC the invention.
XX
SQ Sequence 45 BP; 10 A; 11 C; 14 G; 0 T; 10 U; 0 Other;

Query Match 11.7%; Score 45; DB 13; Length 45;
Best Local Similarity 77.8%; Pred. No. 0.0019;
Matches 35; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

```
Qy        171 GAAUUGCCAGGACGACCGGGUCCUUUCUUGGAUCAACCCGCUCAA 215
              |||::|||||||||||||||:||:::|::|||:|||||||:|||
Db         45 GAATTGCCAGGACGACCGGGTCCTTTCTTGGATCAACCCGCTCAA 1
```

RESULT 6
AAZ23542
ID AAZ23542 standard; DNA; 48 BP.
XX
AC AAZ23542;
XX
DT 21-DEC-1999 (first entry)
XX
DE Human DNA fragment 1.
XX
KW Assay; amplification; hybridisation; probe; detection; viral; bacterial;
KW cellular; yeast; fungal; primer; as

KW cellular; yeast; fungal; primer; ss.
XX
OS Homo sapiens.
XX
PN DE19814828-A1.
XX
PD 07-OCT-1999.
XX
PF 02-APR-1998; 98DE-01014828.
XX
PR 02-APR-1998; 98DE-01014828.
XX
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
XX
PI Kessler C, Haberhausen G, Batz H, Oerum H;
XX
DR WPI; 1999-552286/47.
XX
PT Nucleic acid amplification assay for detecting viral, bacterial,
PT cellular, yeast or fungal nucleic acids.
XX
PS Disclosure; Fig 4; 28pp; German.
XX
CC This invention describes a novel assay for a nucleic acid comprises: (a)
CC generating amplification products from a fragment of the nucleic acid,
CC (b) contacting the amplification products with a probe; and (c) detecting
CC hybridization between the amplification product and the probe. The assay
CC is useful for detection of viral, bacterial, cellular, yeast or fungal
CC nucleic acids in human, animal, bacterial, plant, yeast or fungal
CC samples, e.g. feces, smears, cell suspensions, cultures or tissue, cell
CC or liquid biopsy samples. This sequence represents a fragment of the
CC human genome which is used in the method of the invention
XX
SQ Sequence 48 BP; 9 A; 17 C; 14 G; 8 T; 0 U; 0 Other;

SQ Sequence 48 BP; 9 A; 17 C; 14 G; 8 T; 0 U; 0 Other;

Query Match 11.7%; Score 44.8; DB 2; Length 48;
Best Local Similarity 81.2%; Pred. No. 0.0022;
Matches 39; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

```
Qy          93 AGUAUGAGUGUCGUGCAGCCUCCAGGACCCCCCCUCCCGGGAGAGCCA 140
               ||:|:| |:|:||:||||||:||||||||||| |:|||||||||||||
Db           1 AGTATGTGTGTCGTGCAGCCTCCAGGACCCCCACTCCCGGGAGAGCCA 48
```

RESULT 7
AAV54438
ID AAV54438 standard; DNA; 46 BP.
XX
AC AAV54438;
XX
DT 21-DEC-1998 (first entry)
XX
DE Nucleotide sequence of HCV probe 2.
XX
KW Hepatitis C virus; HCV; probe; hybridisation; ss.
XX
OS Synthetic.
XX
PN JP10248579-A.
XX
PD 22-SEP-1998.
XX
PF 05-MAR-1997; 97JP-00067321.
XX
PR 05-MAR-1997; 97JP-00067321.
XX
PA (TOKB) ZU TOKYOTO RINSHO IGAKU SOGO KENKYUSHO

PA (TOKR-) ZH TOKYOTO RINSHO IGAKU SOGO KENKYUSHO.
PA (SRLS-) SRL KK.
XX
DR WPI; 1998-560731/48.
XX
PT Determination of hepatitis C virus (HCV) gene - with real time detective
PT PCR and primer and probe used for determination.
XX
PS Claim 5; Page 6; 7pp; Japanese.
XX
CC This is the nucleotide sequence of a Hepatitis C virus (HCV) probe, used
CC in the method of the invention. This is a useful for the detection of the
CC HCV gene
XX
SQ Sequence 46 BP; 10 A; 11 C; 14 G; 11 T; 0 U; 0 Other;

Query Match 11.6%; Score 44.4; DB 2; Length 46;
Best Local Similarity 73.9%; Pred. No. 0.0028;
Matches 34; Conservative 11; Mismatches 1; Indels 0; Gaps 0;

```
Qy         74 AGCGUCUAGCCAUGGCGUUAGUAUGAGUGUCGUGCAGCCUCCAGGA 119
              ||||:|:|||||:||||::||:|:|||:|:||:||| ||:||||||
Db          1 AGCGTCTAGCCATGGCGTTAGTATGAGTGTCGTGCAACCTCCAGGA 46
```

RESULT 8
AAA50912
ID AAA50912 standard; DNA; 44 BP.
XX
AC AAA50912;
XX
DT 17-OCT-2000 (first entry)
XX
DE Nucleic acid target sequence for use with trackable optical disks

DE Nucleic acid target sequence for use with trackable optical disks.
XX
KW Probe; trackable optical disk; analyte-specific assay;
KW nucleic acid hybridisation; ss.
XX
OS Synthetic.
XX
PN WO200026677-A1.
XX
PD 11-MAY-2000.
XX
PF 26-OCT-1999; 99WO-US025136.
XX
PR 30-OCT-1998; 98US-00183842.
PR 14-MAY-1999; 99US-00311329.
PR 14-MAY-1999; 99US-0134368P.
XX
PA (BURS-) BURSTEIN LAB INC.
XX
PI Worthington MO, Virtanen J;
XX
DR WPI; 2000-399370/34.
XX
PT Trackable optical disc for confocal laser microscopy has information
PT layer with trackable structure and non-operational structure(s) which all
PT are concurrently readable by single optical pickup.
XX
PS Example 7; Page 90; 154pp; English.
XX
CC A trackable optical disc composed of an information layer with a
CC trackable structure and non-operational structure has been developed for
CC use in confocal laser microscopy. This disc can be used in a nucleic acid
CC -based analyte-specific assay, where specific adherence of a magnetic
CC head to the disc surface is driven by nucleic acid hybridisation. The

```
CC   bead to the disc surface is driven by nucleic acid hybridisation. The
CC   present sequence is a target sequence, which is used in conjunction with
CC   two nucleic acid probes: a 3' probe (AAA50910) and a 5' probe (AAA50911).
CC   The 3' probe was conjugated to a paramagnetic bead via an amino-modified
CC   terminus. The 5' probe was conjugated to biotin. The target sequence is
CC   complementary to the two probes in that the 5' probe captures the 3' end
CC   of the target sequence, and the 3' probe captures the 5' end of the
CC   target, hence the magnetic bead is tethered to the optical disc. The
CC   magnetic bead is then detected by an optical disc reader
XX
SQ   Sequence 44 BP; 9 A; 11 C; 14 G; 10 T; 0 U; 0 Other;

  Query Match             11.5%;  Score 44;  DB 3;  Length 44;
  Best Local Similarity   77.3%;  Pred. No. 0.0037;
  Matches   34;  Conservative   10;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        159 GUGAGUACACCGGAAUUGCCAGGACGACCGGGUCCUUUCUUGGA 202
              |:|||:||||||||::|||||||||||||||:||:::|::|||
Db          1 GTGAGTACACCGGAATTGCCAGGACGACCGGGTCCTTTCTTGGA 44


RESULT 9
ADP87770
ID   ADP87770 standard; DNA; 47 BP.
XX
AC   ADP87770;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Extended primer for TEX detection of Hepatitis C virus #1.
XX
KW   TEX; thermodynamic equilibrium extension of primers; HCV; ss; primer.
XX
OS   Hepatitis C virus
```

OS Hepatitis C virus.
XX
FH Key Location/Qualifiers
FT misc_feature 1. .47
FT /*tag= a
FT /note= "All n are deoxyuridine"
XX
PN US2004115643-A1.
XX
PD 17-JUN-2004.
XX
PF 12-DEC-2002; 2002US-00318416.
XX
PR 12-DEC-2002; 2002US-00318416.
XX
PA (LIZA/) LIZARDI P M.
PA (GRIB/) GRIBANOV O G.
XX
PI Lizardi PM, Gribanov OG;
XX
DR WPI; 2004-468050/44.
XX
PT Amplifying nucleic acid for detecting nucleic acid, by extension of one
PT or more primers using target templates having replication terminating
PT feature, dissociation of primer from templates to produce multiple
PT extended primers.
XX
PS Disclosure; SEQ ID NO 2; 75pp; English.
XX
CC The invention relates to amplifying (M1) a nucleic acid, involving
CC contacting one or more extension primers (EP) and target templates (TT)
CC and incubating under conditions to promote interaction of (EP) and
CC templates, extension of (EP) using the interacting (TT), and dissociation
CC of the extended (EP) from (TT) to produce multiple extended (EP) from at

CC of the extended (EP) from (TT), to produce multiple extended (EP) from at
CC least one (TT), where each (TT) comprise a replication terminating
CC feature. In (M1), (EP) and target templates are incubated under
CC isothermal conditions or single set of conditions. The target templates
CC are nucleic acid sequences of interest. Each of (EP) comprises or
CC consists of a target complement portion, preferably nucleotides, where
CC the nucleotides consist of the target complement portion. Each (EP)
CC further comprises non-target complement portion. The method is known as
CC TEX (thermodynamic equilibrium extension of primers). The method is
CC useful for amplifying nucleic acid and for detecting nucleic acid
CC sequences which involves performing (M1), and detecting one or more of
CC the extended (EP). In (M1), only those sequences targeted by (EP) are
CC amplified, thus allowing specific sequences to be targeted for
CC amplification. Flexibility in the location of replication terminating
CC feature allows flexibility in targeting sequences. If a targeted sequence
CC is not present, the sequence will not be amplified. Multiple sequences
CC can be amplified in the same reaction by targeting multiple sequences
CC with (EP). Simultaneous amplification and detection is facilitated using
CC detection probes associated with a substrate. Multiplex detection can be
CC facilitate by an array of detection probes with different detection
CC probes at different locations of a substrate. The present sequence is a
CC primere used in the TEX method to detect/amplify HCV (Hepatitis C virus)
CC target sequences.
XX
SQ Sequence 47 BP; 11 A; 16 C; 10 G; 6 T; 0 U; 4 Other;

Query Match 11.2%; Score 43; DB 12; Length 47;
Best Local Similarity 78.7%; Pred. No. 0.0075;
Matches 37; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

```
Qy         38 CACUCCCCUGUGAGGAACUACUGUCUUCACGCAGAAAGCGUCUAGCC 84
              ||| |||| | ||||||| ||:|:|::|||||||||||||:|:||||
Db          1 CACNCCCCNGNGAGGAACNACTGTCTTCACGCAGAAAGCGTCTAGCC 47
```

RESULT 10
AAV15321
ID AAV15321 standard; DNA; 42 BP.
XX
AC AAV15321;
XX
DT 25-MAR-2003 (revised)
DT 28-MAY-1998 (first entry)
XX
DE Hepatitis C virus probe 3 CH.
XX
KW Hepatitis C virus; HCV; PCR; detection; reverse transcription; probe;
KW enzyme immunoassay; viral RNA; ss.
XX
OS Synthetic.
OS Hepatitis C virus.
XX
PN WO9746716-A1.
XX
PD 11-DEC-1997.
XX
PF 03-JUN-1997; 97WO-IT000128.
XX
PR 07-JUN-1996; 96IT-RM000404.
XX
PA (WESA) WABCO BV.
XX
PI Bosio P, Strumia C, Clemenza F;
XX
DR WPI; 1998-042222/04.
XX
PT Detection of hepatitis C virus by reverse transcription single step

PT Detection of hepatitis C virus - by reverse transcription, single-step
PT PCR and detection by DNA enzyme immunoassay.
XX
PS Disclosure; Page 4; 26pp; English.
XX
CC The present sequence represents a probe involved in the method of the
CC present invention for detecting hepatitis C virus (HCV). The method
CC comprises: (a) reverse-transcribing the viral RNA; (b) amplifying the
CC resulting cDNA by a single polymerase chain reaction in a reaction
CC mixture having a Mg2+/Taq polymerase ratio of about 100 nmole/enzyme unit
CC ; and (c) detecting the amplification product by DEIA (DNA enzyme
CC immunoassay) using an oligonucleotide probe. The sensitivity of this
CC method is at least equal to that achievable by more complicated assays
CC using nested PCR. (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 42 BP; 8 A; 12 C; 13 G; 9 T; 0 U; 0 Other;

Query Match 11.0%; Score 42; DB 2; Length 42;
Best Local Similarity 78.6%; Pred. No. 0.015;
Matches 33; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

```
Qy        157 CGGUGAGUACACCGGAAUUGCCAGGACGACCGGGUCCUUUCU 198
              |||:|||:|||||||||::|||||||||||||||:||:::|:
Db          1 CGGTGAGTACACCGGAATTGCCAGGACGACCGGGTCCTTTCT 42
```

RESULT 11
AAX60959
ID AAX60959 standard; DNA; 42 BP.
XX
AC AAX60959;
XX
DT 16-AUG-1999 (first entry)

Seq Alignments.
Please Scan + mail

ESULT 33
AAT05222/c
ID AAT05222 standard; DNA; 28 BP.
XX
AC AAT05222;
XX
DT 13-JUN-1996 (first entry)
XX
DE Hepatitis C virus antisense oligonucleotide A312.
XX
KW Inhibition; expression; hepatitis C virus; HCV; non-A; non-B; RNA;
KW translation; in vivo; ex vivo; in vitro; treatment; prevention;
KW infection; antisense; non coding; region; NCR; core region; ss.
XX
OS Synthetic.
XX
PN WO9530746-A1.
XX
PD 16-NOV-1995.
XX
PF 08-MAY-1995; 95WO-US005812.
XX
PR 10-MAY-1994; 94US-00240382.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Wakita T, Wands JR;
XX
DR WPI; 1995-404113/51.
XX
PT New anti:sense hepatitis C virus oligo:nucleotide(s) - used for
PT inhibiting HCV RNA translation, for the treatment or prevention of HCV
PT infection.
XX
PS Claim 1; Page 29; 50pp; English.
XX
CC The present oligonucleotide (ON) inhibits the expression of hepatitis C
CC virus (HCV) RNA, specifically HCV type II and type III protein synthesis
CC is inhibited by 45% and 18%, respectively. The ONs of the invention
CC inhibit translation of HCV types I-V RNA in vivo, ex vivo or in vitro,
CC and can therefore be used to treat or prevent HCV infection. The
CC antisense ONs comprise 10-28 nucleotides complementary to the entire HCV
CC 5'-non-coding and part of the core region. The A or S in the ONs name
CC denotes antisense or sense, and the no. indicates the position of the 5'-
CC end of the ON. The ON was tested at 10 fold molar excess to HCV RNA
XX

SQ Sequence 28 BP; 8 A; 11 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 2; Length 28;
Best Local Similarity 66.7%; Pred. No. 1.3;
Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 GUACUGCCUGAUAGGGUGCUU 21
           |:||:|||:||:||||:||::
Db      27 GTACTGCCTGATAGGGTGCTT 7
```

ESULT 27
AR094974/c
LOCUS AR094974 28 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 12 from patent US 6001990.
ACCESSION AR094974
VERSION AR094974.1 GI:10022401
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 28)
AUTHORS Wands,J.R., Wakita,T. and Moradpour,D.
TITLE Antisense inhibition of hepatitis C virus
JOURNAL Patent: US 6001990-A 12 14-DEC-1999;
FEATURES Location/Qualifiers
source 1. .28
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Query Match 100.0%; Score 21; DB 2; Length 28;
Best Local Similarity 66.7%; Pred. No. 85;
Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GUACUGCCUGAUAGGGUGCUU 21
|:||:|||:||:|||||:||::
Db 27 GTACTGCCTGATAGGGTGCTT 7

RESULT 36
AAZ57757/c
ID AAZ57757 standard; DNA; 28 BP.
XX
AC AAZ57757;
XX
DT 05-APR-2000 (first entry)
XX
DE Hepatitis C virus antisense inhibitor oligonucleotide A312.
XX
KW Hepatitis C virus; HCV; antisense oligonucleotide; hepatotropic; ss;
KW anti-inflammatory; translation inhibition; HCV infection; virucide.
XX
OS Hepatitis C virus.
XX
PN US6001990-A.
XX
PD 14-DEC-1999.
XX
PF 07-JUN-1995; 95US-00474700.
XX
PR 10-MAY-1994; 94US-00240382.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Moradpour D, Wands JR, Wakita T;
XX
DR WPI; 2000-104900/09.
XX
PT Antisense oligonucleotide to Hepatitis C virus RNA, useful for treating
PT Hepatitis C virus infections.
XX
PS Claim 1; Col 23; 31pp; English.
XX
CC This sequence is an antisense oligonucleotide that hybridises to
CC Hepatitis C virus (HCV) RNA, under physiological conditions. The
CC invention relates to HCV antisense oligonucleotides, and also for a
CC vector comprising a nucleotide sequence which is transcribed in an animal
CC cell to generate an antisense oligonucleotide. The oligonucleotides have
CC virucide, hepatotropic and anti-inflammatory activity, and are useful for
CC treating HCV infection by inhibiting translation of type I-V HCV RNA.
CC Hepatitis C virus is a positive strand RNA virus, and is the major
CC causative agent of post-transfusion hepatitis. Persistent HCV infection
CC can lead to chronic hepatitis, cirrhosis, and hepatocellular carcinoma
XX
SQ Sequence 28 BP; 8 A; 11 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 3; Length 28;
Best Local Similarity 66.7%; Pred. No. 1.3;
Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 GUACUGCCUGAUAGGGUGCUU 21
           |:||:||||:||:||||:||::
Db      27 GTACTGCCTGATAGGGTGCTT 7
```

XX

DE Hepatitis C virus (HCV) positive control primer.

XX

KW Nucleic acid detection; pathogen; bacteria; virus; hepatitis C virus;
KW HCV; hepatitis B; HBV; hepatitis G; HGV; HIV; fungus; protozoa; ss;
KW parasite; mycoplasma; genetic mutation; food contamination; PCR primer.

XX

OS Synthetic.
OS Hepatitis C virus.

XX

PN WO9928503-A1.

XX

PD 10-JUN-1999.

XX

PF 16-NOV-1998; 98WO-US024494.

XX

PR 03-DEC-1997; 97IT-RM000749.

XX

PA (DIAS-) DIASORIN INT INC.

XX

PI Primi D, Mantero G;

XX

DR WPI; 1999-371139/31.

XX

PT Detection of single-stranded polynucleotide analytes.

XX

PS Example 12; Page 68; 73pp; English.

XX

CC The invention relates to a new method for detection of single-stranded
CC (ss) polynucleotide analytes that comprises using ss polynucleotide
CC probes which hybridize to the analyte and are bound to a solid support
CC where double-stranded (ds) polynucleotides are detected. The method can
CC be used for detecting ss PN analytes for the detection of pathogens such
CC as bacteria, viruses such as hepatitis C (HCV), hepatitis B (HBV)

```
CC   as bacteria, viruses such as hepatitis C (HCV), hepatitis B (HBV),
CC   hepatitis G (HGV), or HIV, fungi, protozoa, parasites or mycoplasma. The
CC   method can be used to detect the presence of genetic mutations which have
CC   diagnostic or prognostic value. Pathogen contamination of food and drink
CC   supplies can also be detected using the method. The method provides for
CC   the sensitive and specific detection of ss PN analytes at concentration
CC   as low as 0.1fg
XX
SQ   Sequence 42 BP; 8 A; 12 C; 13 G; 9 T; 0 U; 0 Other;

  Query Match             11.0%;  Score 42;  DB 2;  Length 42;
  Best Local Similarity   78.6%;  Pred. No. 0.015;
  Matches   33;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        157 CGGUGAGUACACCGGAAUUGCCAGGACGACCGGGUCCUUUCU 198
              |||:|||:|||||||||::|||||||||||||||:||:::|:
Db          1 CGGTGAGTACACCGGAATTGCCAGGACGACCGGGTCCTTTCT 42


RESULT 12
AEF39282
ID   AEF39282 standard; DNA; 42 BP.
XX
AC   AEF39282;
XX
DT   23-MAR-2006  (first entry)
XX
DE   HCV 224 targeted DNA fragment SEQ ID NO 40.
XX
KW   ds; enzyme engineering; DNA cleavage; ribonuclease; ribozyme delta;
KW   RNA cleavage.
XX
OS   Hepatitis C virus.
XX
```

XX

PN WO2006002547-A1.

XX

PD 12-JAN-2006.

XX

PF 06-JUL-2005; 2005WO-CA001051.

XX

PR 06-JUL-2004; 2004US-0585093P.

XX

PA (UYSH) UNIV SHERBROOKE.

XX

PI Perreault J, Bergeron L;

XX

DR WPI; 2006-090285/09.

XX

PT New target-dependent nucleic acid adapter comprising a blocker stem
PT sequence or a biosensor sequence, useful for improving specificity of a
PT nucleic acid sequence for a target sequence.

XX

PS Disclosure; SEQ ID NO 40; 145pp; English.

XX

CC This invention describes a novel target-dependent nucleic acid adapter,
CC to be matched to a substrate comprising a target sequence, has a nucleic
CC acid sequence comprising: a blocker stem sequence complementary to a
CC portion of the sequence and a biosensor sequence having a sequence
CC complementary to the target sequence and improving the specificity of the
CC sequence for the target sequence. In the absence of the target sequence
CC of the substrate, the blocker stem sequence forms an intramolecular stem
CC with the nucleic acid sequence linked to it, preventing exposition of the
CC nucleic acid sequence; thus locking the nucleic acid sequence of the
CC adapter in an inactive conformation. In the presence of target sequence
CC of the substrate, the biosensor sequence forms conventional Watson-Crick
CC base pairs with the target sequence and the blocker stem sequence
CC dissociates from the intramolecular stem; thus exposing the nucleic acid

CC dissociates from the intramolecular stem; thus exposing the nucleic acid
CC sequence of the adapter in an active conformation. The invention also
CC describes a) a method for improving specificity of a nucleic acid
CC sequence for a target sequence; b) a method for turning on or off
CC enzymatic activity of a nucleic acid molecule having an enzymatic
CC activity, which comprises attaching to the nucleic acid molecule the
CC target-dependent nucleic acid adapter and c) a target-specific
CC activatable/deactivatable ribonuclease adapted to be matched to a
CC substrate comprising a target sequence. The target-dependent nucleic acid
CC adapter further comprises a nucleic acid sequence forming a stabilizing
CC stem, where the 3' end of the nucleic acid sequence of the adapter is
CC paired up with the nucleic acid sequence, forming an intramolecular stem
CC at the 3' end of the nucleic acid sequence, thus preventing or reducing
CC degradation of the nucleic acid sequence. The stabilizing stem has two
CC complementary strands, a first strand of which is linked to the 5' end of
CC the biosensor sequence, and a second strand of which is complementary to
CC the first strand and is adapted to be linked at its 5' end to the 3' end
CC of the nucleic acid sequence; thus preventing exposure of a single
CC stranded 3' end sequence susceptible to degradation by cellular nuclease.
CC The blocker stem sequence has a sequence specific for a ribozyme delta
CC and is linked to the biosensor. The target-dependent nucleic acid adapter
CC is useful for improving specificity of a nucleic acid sequence for a
CC target sequence or for turning on or off an enzymatic activity of a
CC nucleic acid molecule having an enzymatic activity. This sequence
CC represents a fragment of HCV 224 which is a target for the ribozymes of
CC the invention.
XX
SQ Sequence 42 BP; 7 A; 11 C; 15 G; 9 T; 0 U; 0 Other;

Query Match 11.0%; Score 42; DB 15; Length 42;
Best Local Similarity 78.6%; Pred. No. 0.015;
Matches 33; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

Qy 223 ACAUUUGCCCCUCCCCCCCCCACACUCCUACCCCACUACUCU 264

```
Qy         223 AGAUUUGGGCGUGCCCCCGCGAGACUGCUAGCCGAGUAGUGU 264
               |||:::||||||||||||||||||:||:|||||||:||:|:
Db           1 AGATTTGGGCGTGCCCCCGCGAGACTGCTAGCCGAGTAGTGT 42
```

RESULT 13
ADW28911
ID ADW28911 standard; DNA; 49 BP.
XX
AC ADW28911;
XX
DT 24-MAR-2005 (first entry)
XX
DE Wild type hepatitis C virus type 1a (H) core+1 DNA oligo Seq 25.
XX
KW hepatitis C virus infection; immunogenic; antibody production;
KW protein engineering; virucide; ds; screening.
XX
OS Hepatitis C virus type 1a.
XX

FH	Key	Location/Qualifiers
FT	CDS	1. .48
FT		/*tag= a
FT		/partial
FT		/product= "HCV1a core+1 peptide"
FT		/note= "Stop codon is absent"

XX
PN EP1493749-A1.
XX
PD 05-JAN-2005.
XX
PF 04-JUL-2003; 2003EP-00291676.
XX
PR 04-JUL-2003; 2003EP-00291676

PR 04-JUL-2003; 2003EP-00291676.
XX
PA (INSP) INST PASTEUR.
PA (INSP) INST PASTEUR HELLENIQUE.
XX
PI Mavromara P, Niki V;
XX
DR WPI; 2005-067632/08.
DR P-PSDB; ADW28912.
XX
PT Novel shorter form core+1 protein of hepatitis C virus, useful for in
PT vitro method for detection of infection by HCV or for preparing
PT immunogenic composition against HCV infection.
XX
PS Disclosure; SEQ ID NO 25; 80pp; English.
XX
CC This invention relates to a novel Hepatitis C virus (HCV) core+1 protein
CC that can be used to elicit a CTL response against HCV infection.
CC Specifically, it refers to a truncated form of the core+1 protein that is
CC the product of translation of a coding sequence that consists of all or a
CC portion of the nucleotide sequence extending from nucleotide 598-920
CC within the core+1 open reading frame (ORF) of HCV. The present invention
CC describes engineered mutations designed to introduce premature stop
CC codons and hence generate various truncated core+1 HCV proteins that can
CC be used for preparing immunogenic compositions against HCV infection i.e.
CC as antigens for the production of HCV antibodies. Accordingly, it
CC provides an in vitro method useful for the detection of HCV infection
CC that involves determining the presence of these antibodies, in particular
CC antigen-antibody complexes can be detected by immunoassay (direct
CC detection) or ELISA (indirect detection). Furthermore, it refers to a
CC screening method to identify virucidal compounds that interact with viral
CC propagation in cells infected by HCV, such that successful compounds can
CC be used in the preparation of a medicine for the treatment of disorders
CC induced by or associated with HCV infection. This oligonucleotide

```
CC   induced by or associated with HCV infection. This oligonucleotide
CC   sequence is a wild type HCV type 1a core+1 DNA fragment of the invention.
XX
SQ   Sequence 49 BP; 24 A; 15 C; 5 G; 5 T; 0 U; 0 Other;

  Query Match             11.0%;  Score 42;  DB 14;  Length 49;
  Best Local Similarity   88.1%;  Pred. No. 0.015;
  Matches   37;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        342 AUGAGCACGAAUCCUAAACCUCAAAGAAAAACCAAACGUAAC 383
              |:|||||||||:||:|||||:||||||||||||||||:|||
Db          1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAAC 42


RESULT 14
AAT09177/c
ID   AAT09177 standard; DNA; 45 BP.
XX
AC   AAT09177;
XX
DT   21-OCT-2004  (revised)
DT   14-AUG-1996  (first entry)
XX
DE   Hepatitis C virus specific capture/amp-probe-1A (HCV A).
XX
KW   Ligase dependent polymerase chain reaction; LD-PCR; probe; hybridisation;
KW   ligand binding pair; ligase; paramagnetic bead; primer; amplification;
KW   hepatitis; untranslated region; UTR; rRNA; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_binding     5. .45
FT                    /tag= a
```

FT /*tag= a
FT /bound_moiety
FT /note= "complementary to Hepatitis C virus 5'
FT untranslated region"
XX
PN WO9535390-A1.
XX
PD 28-DEC-1995.
XX
PF 14-JUN-1995; 95WO-US007671.
XX
PR 22-JUN-1994; 94US-00263937.
XX
PA (MOUN) MOUNT SINAI SCHOOL MEDICINE.
XX
PI Zhang DY;
XX
DR WPI; 1996-058427/06.
XX
PT Ligation dependent polymerase chain reaction - for the detection of
PT infectious pathogens and abnormal human genes, e.g. HIV and neoplasia.
XX
PS Claim 47; Page 53; 100pp; English.
XX
CC A novel method of detecting a target nucleic acid (TNA) sequence involves
CC use of the ligase dependent polymerase chain reaction method (LD-PCR). In
CC this method, two probes are provided. The first probe contains a region
CC at the 5' end which is complementary and will hybridise with the TNA, the
CC 3' end of the first probe is generic and is bound to one half of a ligand
CC binding pair (LBP). The second probe contains a region at the 5' end
CC which is complementary to a region in the TNA which is immediately
CC adjacent to the complementary region of the first probe. When the probes
CC are bound to the TNA, they can be ligated together using a conventional
CC ligase. The TNA:ligated probe complex can be isolated by binding the

```
CC   ligase. The TNA:ligated probe complex can be isolated by binding the
CC   first probe to a paramagnetic bead to which is attached the second half
CC   of the LBP. The TNA can be dissociated from the ligated probe complex
CC   which can then be detected either by a label attached to the second
CC   probe, by using an external probe or by PCR using the ligated probes as a
CC   template. The capture probes AAT09176-7 are used to isolated a region of
CC   the Hepatitis C virus 5' untranslated region. This region can then be
CC   detected by the probes AAT09178-9 to produce the ligated amplification
CC   sequence AAT09180. The ligated sequence can subsequently be detected by
CC   PCR amplification with the primers AAT09181-3
CC
CC   Revised record issued on 21-OCT-2004 : Correction to Feature Table Key
XX
SQ   Sequence 45 BP; 11 A; 16 C; 12 G; 6 T; 0 U; 0 Other;

  Query Match             10.8%;  Score 41.4;  DB 2;  Length 45;
  Best Local Similarity   76.7%;  Pred. No. 0.022;
  Matches   33;  Conservative    9;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        228 UGGGCGUGCCCCCGCGAGACUGCUAGCCGAGUAGUGUUGGGUC 270
              :|||||:|||||||| |||||:||:|||||||:||:|::|||:|
Db         45 TGGGCGTGCCCCCGCAAGACTGCTAGCCGAGTAGTGTTGGGTC 3


RESULT 15
AAV20718/c
ID   AAV20718 standard; DNA; 45 BP.
XX
AC   AAV20718;
XX
DT   17-JUL-1998  (first entry)
XX
DE   Hepatitis C virus probe SEQ ID NO:23.
XX
```

XX

KW Hepatitis C virus; HCV; HIV; probe; detection; capture; amplification;
KW paramagnetic particle; ligation; ss.

XX

OS Synthetic.
OS Hepatitis C virus.

XX

PN WO9804745-A1.

XX

PD 05-FEB-1998.

XX

PF 30-JUL-1997; 97WO-US013390.

XX

PR 31-JUL-1996; 96US-00690495.

XX

PA (MOUN) MOUNT SINAI SCHOOL MEDICINE.

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PI Zhang DY, Brandwein M;

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DR WPI; 1998-159153/14.

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PT Detection of target nucleic acids in samples - using capture and
PT amplification probes, paramagnetic particles and ligation to form a
PT nucleotide sequence which can be detected.

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PS Example 4; Page 62; 136pp; English.

XX

CC The present sequence represents a probe used in an example of the present
CC invention for the detection of HCV RNA in a sample. The present invention
CC describes methods for: (A) detecting a target nucleic acid (NA) in a
CC sample; (B) in situ detection of a target NA in a sample; (C) detecting
CC an antigen in a sample; and (D) detecting an antibody in a sample. The
CC methods can be used for the rapid automated detection and monitoring of
CC pathogenic organisms, as well as the detection of abnormal genes in an

CC pathogenic organisms, as well as the detection of abnormal genes in an
CC individual. The methods allow for isolation, amplification and detection
CC of NA sequences corresponding to the target NA to be carried out in the
CC same receptacle, e.g. tube or micro-well plate. The method also allows
CC for standardisation of conditions, because only a pair of generic
CC amplification probes may be utilised in the present method for detecting
CC a variety of target NAs, thus allowing efficient multiplex amplification.
CC The method also allows the direct detection of RNA by probe amplification
CC without the need for DNA template production. The amplification probes,
CC which may be covalently joined end to end, form a contiguous ligated
CC amplification sequence. The assembly of the amplifiable DNA by ligation
CC increase specificity, and makes possible the detection of a single
CC mutation in a target
XX
SQ Sequence 45 BP; 11 A; 16 C; 12 G; 6 T; 0 U; 0 Other;

Query Match 10.8%; Score 41.4; DB 2; Length 45;
Best Local Similarity 76.7%; Pred. No. 0.022;
Matches 33; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

```
Qy        228 UGGGCGUGCCCCCGCGAGACUGCUAGCCGAGUAGUGUUGGGUC 270
              :|||||:|||||||| |||||:||:|||||||:||:|::||||:|
Db         45 TGGGCGTGCCCCCGCAAGACTGCTAGCCGAGTAGTGTTGGGTC 3
```

Search completed: September 21, 2007, 14:29:16
Job time : 445 secs

GenCore version 6.2.1

OM nucleic - nucleic search, using sw model

Run on: December 5, 2007, 15:31:59 ; Search time 372 Seconds
(without alignments)
609.417 Million cell updates/sec

Title: US-10-626-879-1
Perfect score: 21
Sequence: 1 guacugccugauagggugcuu 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9073515 seqs, 5397694045 residues

Total number of hits satisfying chosen parameters: 8735976

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : N_Geneseq_200711:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000:*
4: geneseqn2001s:*

4: geneseqn2001a:*
5: geneseqn2001b:*
6: geneseqn2002a:*
7: geneseqn2002b:*
8: geneseqn2003a:*
9: geneseqn2003b:*
10: geneseqn2003c:*
11: geneseqn2003d:*
12: geneseqn2004a:*
13: geneseqn2004b:*
14: geneseqn2004c:*
15: geneseqn2004d:*
16: geneseqn2005a:*
17: geneseqn2005b:*
18: geneseqn2005c:*
19: geneseqn2006a:*
20: geneseqn2006b:*
21: geneseqn2006c:*
22: geneseqn2007:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	21	100.0	21	12	ADJ38935	Adj38935 Hepatitis
2	21	100.0	21	16	ADY75012	Ady75012 Hepatitis
3	21	100.0	21	16	ADZ02291	Adz02291 Hepatitis
4	21	100.0	21	16	ADZ02349	Adz02349 Hepatitis
5	21	100.0	21	16	AEC61919	Aec61919 Hepatitis

	5	21	100.0	21	16	AEC61919	Aec61919 Hepatitis
	6	21	100.0	21	16	AEC61977	Aec61977 Hepatitis
	7	21	100.0	21	19	AEG73671	Aeg73671 HCV 5' UT
	8	21	100.0	21	19	AEG96040	Aeg96040 Hepatitis
	9	21	100.0	21	19	AEI66282	Aei66282 Hepatitis
	10	21	100.0	21	19	AEK46630	Aek46630 HCV modif
	11	21	100.0	21	19	AEK46688	Aek46688 HCV modif
	12	21	100.0	23	10	ADF52816	Adf52816 Hepatitis
	13	21	100.0	23	10	ADF52817	Adf52817 Hepatitis
	14	21	100.0	23	10	ADF52973	Adf52973 Hepatitis
	15	21	100.0	23	10	ADF52915	Adf52915 Hepatitis
	16	21	100.0	23	16	ADZ02137	Adz02137 Hepatitis
	17	21	100.0	23	16	ADZ02138	Adz02138 Hepatitis
	18	21	100.0	23	16	ADZ02173	Adz02173 Hepatitis
	19	21	100.0	23	16	AEC61765	Aec61765 Hepatitis
	20	21	100.0	23	16	AEC61766	Aec61766 Hepatitis
	21	21	100.0	23	16	AEC61801	Aec61801 Hepatitis
	22	21	100.0	23	19	AEK46476	Aek46476 HCV targe
	23	21	100.0	23	19	AEK46477	Aek46477 HCV targe
	24	21	100.0	23	19	AEK46512	Aek46512 HCV targe
c	25	21	100.0	24	5	AAD19057	Aad19057 Hepatitis
c	26	21	100.0	27	2	AAT67195	Aat67195 Hepatitis
c	27	21	100.0	27	3	AAZ87367	Aaz87367 Hepatitis
c	28	21	100.0	27	3	AAA74623	Aaa74623 HCV-speci
c	29	21	100.0	27	5	AAH78439	Aah78439 PCR prime
c	30	21	100.0	27	5	AAH78441	Aah78441 PCR prime
	31	21	100.0	27	19	AEG73676	Aeg73676 HCV 5' UT
	32	21	100.0	27	19	AEI66298	Aei66298 Hepatitis
c	33	21	100.0	28	2	AAT05222	Aat05222 Hepatitis
c	34	21	100.0	28	2	AAT67194	Aat67194 Hepatitis
c	35	21	100.0	28	2	AAV59059	Aav59059 Primer ST
c	36	21	100.0	28	3	AAZ57757	Aaz57757 Hepatitis
c	37	21	100.0	28	4	AAH25414	Aah25414 Reverse P
c	38	21	100.0	28	10	ADC84693	Adc84693 PCR prime

c	38	21	100.0	28	10	ADC84693	Adc84693 PCR prime
c	39	21	100.0	28	22	AER42522	Aer42522 HCV RNA a
c	40	21	100.0	28	22	AES98404	Aes98404 Hepatitis
c	41	21	100.0	28	22	AFK91236	Afk91236 Hepatitis
c	42	21	100.0	29	6	AAD43740	Aad43740 HCV DNA a
c	43	21	100.0	29	6	AAD43288	Aad43288 HCV DNA a
	44	21	100.0	29	9	ADC54073	Adc54073 HCV 5'UTR
c	45	21	100.0	30	2	AAQ55728	Aaq55728 Hepatitis
c	46	21	100.0	30	22	AFY25780	Afy25780 HCV RNA R
c	47	21	100.0	33	2	AAQ31158	Aaq31158 Probe 127
c	48	21	100.0	33	2	AAQ46464	Aaq46464 Hepatitis
c	49	21	100.0	33	2	AAV07838	Aav07838 HCV.33.9
c	50	21	100.0	33	2	AAV83066	Aav83066 Amplifier
c	51	21	100.0	40	2	AAV54436	Aav54436 Nucleotid
	52	20	95.2	21	16	ADZ02350	Adz02350 Hepatitis
	53	20	95.2	21	16	ADZ02292	Adz02292 Hepatitis
	54	20	95.2	21	16	AEC61920	Aec61920 Hepatitis
	55	20	95.2	21	16	AEC61978	Aec61978 Hepatitis
	56	20	95.2	21	19	AEG73674	Aeg73674 HCV 5' UT
	57	20	95.2	21	19	AEI66297	Aei66297 Hepatitis
	58	20	95.2	21	19	AEK46631	Aek46631 HCV modif
	59	20	95.2	21	19	AEK46689	Aek46689 HCV modif
	60	20	95.2	23	10	ADF52916	Adf52916 Hepatitis
	61	20	95.2	23	10	ADF52974	Adf52974 Hepatitis
	62	20	95.2	23	10	ADF52815	Adf52815 Hepatitis
	63	20	95.2	23	10	ADF52818	Adf52818 Hepatitis
	64	20	95.2	23	16	ADZ02136	Adz02136 Hepatitis
	65	20	95.2	23	16	ADZ02139	Adz02139 Hepatitis
	66	20	95.2	23	16	AEC61764	Aec61764 Hepatitis
	67	20	95.2	23	16	AEC61767	Aec61767 Hepatitis
	68	20	95.2	23	19	AEK46475	Aek46475 HCV targe
	69	20	95.2	23	19	AEK46478	Aek46478 HCV targe
	70	20	95.2	25	19	AEG73678	Aeg73678 HCV 5' UT
	71	20	95.2	25	19	AEI66299	Aei66299 Hepatitis

	71	20	95.2	25	19	AEI66299	Aei66299 Hepatitis
c	72	20	95.2	27	2	AAQ71839	Aaq71839 PCR prime
c	73	20	95.2	27	3	AAA74624	Aaa74624 HCV-speci
c	74	20	95.2	27	5	ABK09262	Abk09262 Enzymatic
	75	20	95.2	27	5	ABK09264	Abk09264 Enzymatic
c	76	20	95.2	27	5	ABA02736	Aba02736 Nucleic a
	77	20	95.2	27	5	ABA02738	Aba02738 Nucleic a
	78	19	90.5	19	10	ADF51425	Adf51425 Hepatitis
	79	19	90.5	19	10	ADF51419	Adf51419 Hepatitis
	80	19	90.5	19	10	ADF51426	Adf51426 Hepatitis
c	81	19	90.5	19	10	ADF52115	Adf52115 Hepatitis
c	82	19	90.5	19	10	ADF52121	Adf52121 Hepatitis
c	83	19	90.5	19	10	ADF52122	Adf52122 Hepatitis
c	84	19	90.5	19	16	ADZ01443	Adz01443 Hepatitis
	85	19	90.5	19	16	ADZ00746	Adz00746 Hepatitis
	86	19	90.5	19	16	ADZ00747	Adz00747 Hepatitis
	87	19	90.5	19	16	ADZ00740	Adz00740 Hepatitis
c	88	19	90.5	19	16	ADZ01436	Adz01436 Hepatitis
c	89	19	90.5	19	16	ADZ01442	Adz01442 Hepatitis
	90	19	90.5	19	16	AEC60368	Aec60368 Hepatitis
	91	19	90.5	19	16	AEC60374	Aec60374 Hepatitis
	92	19	90.5	19	16	AEC60375	Aec60375 Hepatitis
c	93	19	90.5	19	16	AEC61064	Aec61064 Hepatitis
c	94	19	90.5	19	16	AEC61070	Aec61070 Hepatitis
c	95	19	90.5	19	16	AEC61071	Aec61071 Hepatitis
	96	19	90.5	19	19	AEK45079	Aek45079 HCV targe
	97	19	90.5	19	19	AEK45085	Aek45085 HCV targe
	98	19	90.5	19	19	AEK45086	Aek45086 HCV targe
c	99	19	90.5	19	19	AEK45775	Aek45775 HCV siRNA
c	100	19	90.5	19	19	AEK45781	Aek45781 HCV siRNA
c	101	19	90.5	19	19	AEK45782	Aek45782 HCV siRNA
c	102	19	90.5	21	5	ABA03376	Aba03376 Human gen
c	103	19	90.5	21	10	ADF52987	Adf52987 Hepatitis
c	104	19	90.5	21	10	ADF52985	Adf52985 Hepatitis

c 104	19	90.5	21	10	ADF52985	Adf52985 Hepatitis
c 105	19	90.5	21	10	ADF52927	Adf52927 Hepatitis
c 106	19	90.5	21	10	ADF52986	Adf52986 Hepatitis
c 107	19	90.5	21	10	ADF52928	Adf52928 Hepatitis
c 108	19	90.5	21	10	ADF52929	Adf52929 Hepatitis
c 109	19	90.5	21	12	ADJ38936	Adj38936 Hepatitis
110	19	90.5	21	13	ADV97471	Adv97471 Hepatitis
111	19	90.5	21	13	ADV97441	Adv97441 Hepatitis
c 112	19	90.5	21	16	ADY75013	Ady75013 Hepatitis
c 113	19	90.5	21	16	ADZ02363	Adz02363 Hepatitis
c 114	19	90.5	21	16	ADZ02565	Adz02565 Hepatitis
115	19	90.5	21	16	ADZ02525	Adz02525 Hepatitis
c 116	19	90.5	21	16	ADZ02304	Adz02304 Hepatitis
c 117	19	90.5	21	16	ADZ02305	Adz02305 Hepatitis
c 118	19	90.5	21	16	ADZ02303	Adz02303 Hepatitis
c 119	19	90.5	21	16	ADZ02361	Adz02361 Hepatitis
c 120	19	90.5	21	16	ADZ02362	Adz02362 Hepatitis
121	19	90.5	21	16	AEC62153	Aec62153 Hepatitis
c 122	19	90.5	21	16	AEC62193	Aec62193 Hepatitis
c 123	19	90.5	21	16	AEC61931	Aec61931 Hepatitis
c 124	19	90.5	21	16	AEC61932	Aec61932 Hepatitis
c 125	19	90.5	21	16	AEC61933	Aec61933 Hepatitis
c 126	19	90.5	21	16	AEC61989	Aec61989 Hepatitis
c 127	19	90.5	21	16	AEC61990	Aec61990 Hepatitis
c 128	19	90.5	21	16	AEC61991	Aec61991 Hepatitis
c 129	19	90.5	21	17	AED25029	Aed25029 Short int
c 130	19	90.5	21	17	AED24897	Aed24897 Short int
c 131	19	90.5	21	19	AEK77228	Aek77228 Hepatitis
c 132	19	90.5	21	19	AEK94843	Aek94843 HCV targe
c 133	19	90.5	21	19	AEK46642	Aek46642 HCV modif
c 134	19	90.5	21	19	AEK46643	Aek46643 HCV modif
c 135	19	90.5	21	19	AEK46644	Aek46644 HCV modif
c 136	19	90.5	21	19	AEK46700	Aek46700 HCV modif
c 137	19	90.5	21	19	AEK46701	Aek46701 HCV modif

c 137	19	90.5	21	19	AEK46701	Aek46701 HCV modif
c 138	19	90.5	21	19	AEK46702	Aek46702 HCV modif
139	19	90.5	21	19	AEK46864	Aek46864 HCV modif
c 140	19	90.5	21	19	AEK46904	Aek46904 HCV modif
c 141	19	90.5	21	19	AEK78214	Aek78214 Gene expr
c 142	19	90.5	21	19	AEK62155	Aek62155 Exemplary
c 143	19	90.5	21	19	AEK69542	Aek69542 HCV antis
c 144	19	90.5	21	22	AEM47364	Aem47364 HCVa siRN
c 145	19	90.5	21	22	AEM83887	Aem83887 HCV siRNA
c 146	19	90.5	21	22	AEM84484	Aem84484 HCV siRNA
c 147	19	90.5	21	22	AEM92565	Aem92565 HCV siRNA
c 148	19	90.5	21	22	AEM91738	Aem91738 HCV siRNA
c 149	19	90.5	22	19	AEF57898	Aef57898 Hepatitis
c 150	19	90.5	22	22	AFL01190	Afl01190 Antisense
c 151	19	90.5	23	2	AAQ53257	Aaq53257 Hepatitis
152	19	90.5	23	10	ADF52814	Adf52814 Hepatitis
153	19	90.5	23	10	ADF52819	Adf52819 Hepatitis
154	19	90.5	23	16	ADZ02140	Adz02140 Hepatitis
155	19	90.5	23	16	ADZ02135	Adz02135 Hepatitis
156	19	90.5	23	16	AEC61763	Aec61763 Hepatitis
157	19	90.5	23	16	AEC61768	Aec61768 Hepatitis
158	19	90.5	23	19	AEK46474	Aek46474 HCV targe
159	19	90.5	23	19	AEK46479	Aek46479 HCV targe
c 160	19	90.5	24	2	AAQ37586	Aaq37586 HCV conse
161	19	90.5	24	2	AAQ43144	Aaq43144 HCV core
c 162	19	90.5	24	2	AAQ79963	Aaq79963 Primer KY
c 163	19	90.5	24	2	AAT64900	Aat64900 Hepatitis
c 164	19	90.5	24	2	AAT87095	Aat87095 HCV gene
c 165	19	90.5	24	2	AAT93542	Aat93542 Antisense
c 166	19	90.5	24	2	AAV15319	Aav15319 Hepatitis
c 167	19	90.5	24	2	AAV18850	Aav18850 Primer KY
c 168	19	90.5	24	2	AAX23969	Aax23969 PCR prime
c 169	19	90.5	24	2	AAX78452	Aax78452 HCV PCR p
c 170	19	90.5	24	2	AAZ09708	Aaz09708 HCV PCR p

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